

**FIGURE 1**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGCTTCAGCCTGA  
AGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCTTGGCCTCCAACTTGTGGG  
CTACATCCTAGGCCTCTGGGCTTTGGGCACACTGGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTA  
TGTCGGTGCCAGCATTGTGACAGCAGTGGCTCTCCAAGGGCTCTGGATGGAATGTGCCACACACAGCACAGG  
CATCACCCAGTGTGACATCTATAGCACCCCTCTGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGATGGT  
GACATCCAGTGCAATCTCCCTGGCCTGCATTATCTCTGTGGTGGCATGAGATGCACAGTCTTCTGCCAGGA  
ATCCCGAGCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTCATCCTGGAGGCCTCTGGATTCAATTCC  
TGTTGCCTGGAATCTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAGCATGAAATTGAGAT  
TGGAGAGGCCTTTACTGGGCATTATTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTG  
CTCATCCCAGAGAAATCGCTCCAACTAACGATGCCAACCTCTGCCACAAGGAGCTCTCCAAG  
GCCTGGTCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGTATGTGTAAGAACCAGGG  
CCAGAGCTGGGGGTGGCTGGCTGTGAAAAACAGTGGACAGCACCCGAGGCCACAGGTGAGGGACACTACC  
ACTGGATCGTGTCAAGAGGTGCTGCTGAGGATAGACTGACTTGGCATTGGATTGAGCAAAGGCAGAAATGGGG  
GCTAGTGTAAACAGCATGCAAGGTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTTCCTCACCTGCT  
GCTCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCAGGACTCAGAGGATCCCTTG  
CCCTCTGGTTACCTGGACTCCATCCCCAACCCACTAATCACATCCCACGTGACTGACCCCTGTGATCAAAGA  
CCCTCTCTGGCTGAGGTTGGCTCTAGCTATTGCTGGGATGGAAGGAGAACGAGTGGCTTTGTGGCAT  
TGCTCTAACCTACTTCTCAAGCTCCCTCAAAGAAACTGATTGGCCTGGAACCTCCACTCCACTCTGTTATG  
ACTCCACAGTGTCCAGACTAATTGTGCACTGAAATAAAACCATCCTACGGTATCCAGGAAACAGAAAGCA  
GGATGCAGGATGGGAGGACAGGAAGGCAGCCTGGACATTAAAAAAATA

**FIGURE 2**

GAGAGAGGCAGCAGCTGCTCAGCGAACAGGATGCTGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGGCCT  
 CCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGCCAGGCCAGGACCTGTGAGGGAGGCCCTCCTGCTGC  
 CTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTG  
 ACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGAACACCCGTATCCCCATGGAGACCTTCAGAA  
 AGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTTGTCTCATCAAGGTGA  
 TTCTGGATAAATACTACTTCCTCTGCAGGCCTCCACTTCATCCCCAGGAAGCAGCTGTGACGGAGAGC  
 TGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAGAGCTTCCAGGCCACAGGAACACTGGTTCTGCCTGTTGACA  
 TCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGAACACTGGTTCTGCCTGTTGACA  
 TCACAGAAGCTCGCTGAGACAGCCTGTAGGCAGATGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGG  
 ATCTGGATGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGATGCGGAACACTCAAGTGGCCCTGTCTCAG  
 GCTCCCTGGTCTCCCTGCACTGTCTGCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGAGGAGG  
 CCTCTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGG  
 ACCCCCCACTGGGCCTCACGGCAGCCCAGTCTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCCAGG  
 GCTCAGACAAACTGGCAGCTTCCATCCCTGGCTGTGGCAAGATCATCATCATTGAATTCAACCCATGTACC  
 CCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCACTCACTTCTCAGGCACAGTCAGGCCATCTGTC  
 TGCCCTTCTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGATGGGCTTACGAAGCAGAAATG  
 GAGGGAAAGATGTCGACATACTGCTGCAGGCGTCAGTCCAGGTGATTGACAGCACACGGTCAATGCAGACGATG  
 CGTACCAAGGGGAAGTCACCGAGAAGATGATGTGTCAGGCATCCGGAAAGGGGGTGTGGACACCTGCCAGGGTG  
 ACAGTGGTGGGCCCTGATGTACCAATCTGACCAAGTGGCATGTGGTGGCATCGTAGCTGGGCTATGGCTGCG  
 GGGGCCGAGCACCCAGGAGTATAACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTG  
AGCTGTAATGCTGCTGCCCTTGCAGTGCTGGAGCCGCTTCCCTGCCCTGCCACCTGGGATCCCCAA  
 AGTCAGACACAGAGCAAGAGTCCCCTGGTACACCCCTGCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAG  
 GGCCCTCAATTCTGTAAAGAGACCCCTCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTGCCACAC  
 TTGGTGCTCCAGCATCCAGGGAGAGACACAGCCCAGTGAACAAGGTCTCAGGGTATTGCTAAGCCAAGAAGG  
 AACCTTCCACACTACTGAATGGAAGCAGGCTGTTGTAAGGCCCAGATCACTGTGGCTGGAGAGGAGAAGG  
 AAAGGGTCTGCGCCAGCCCTGTCGTCTCACCCATCCCCAGCCTACTAGAGCAAGAAACCAGTTGTAATATAA  
 AATGCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCATTGTTATTACAGCTATGCCACTATTA  
 TAAAGAGCTGTGTAACATCTGGCAAAAAAAAAAA

### **FIGURE 3**

GGAGGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACTGGCTGGGAACCTCCCCAGCCATGGCTTCCCTGGG  
CAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTGGT  
ATTTCAAGGAGACACTCCATCACAGTCACTACTGTCGCCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGC  
TGCACCTTGAAACCTGACATCAAACCTTCTGATATCGTACAGATACTGGCTGAAGGAAGGTGTTTAGGCTTGTC  
CATGAGTTCAAAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTAGGGCCGGACAGCAGTGTGCT  
GATCAAGTGATAGTGGCAATGCCCTTTGGCTGAAAAACGTGCAAACACAGATGCTGGCACCTACAAATGT  
TATATCATCACTCTAAAGGCAAGGGGATGCTAACCTTGAGTATAAAACTGGAGCCTTCAGCATGCCGGAAAGTG  
AATGTGGACTATAATGCCAGCTCAGAGACCTTGGGTGTGAGGCTCCCCGATGGTCCCCCAGCCCACAGTGGTC  
TGGGCATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATACCAGCTTGAGCTGAACCTGAGAAT  
GTGACCATGAAGGTTGTCTGTGCTACAATGTTACGATCAACAAACACATACTCCTGTATGATTGAAAATGAC  
ATTGCCAAAGCAACAGGGATATCAAAGTGACAGAACTGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAC  
TCAAAGGCTCTGTGTCTTCTTCTTGCCATCAGCTGGCACTTCTGCCTCTAGCCCTTACCTGATG  
CTAAAATAGTGCCTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCAC  
CACCAGATATGACCTAGTTATATTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAAG  
AGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCAAATATGAACAAAGATAATCTATCTCAAAGACATATTA  
GAAGTTGGGAAAATAATTGATGTGAAGTCAAGTGTTAAGAGTGATAAGTAAATGCACGTGGAGACAAGT  
GCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGGAGTGAGAGGGACAGGATAGTCATGTTCTTG  
TCTCTGAATTAGTTATGTGCTGTAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCAAACATATCCA  
CATCTTATATTCCACAAATTAGCTGTAGTATGTAACCTAAAGACGCTGCTAATTGACTGCCACTCGCAACTCAG  
GGGCGGCTGCATTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCAAAGGTGCCTGGCTCTTC  
CCAAGTGCACAAATGCCAAAGTTGAGAAAAATGATCATATTAGCATAAACAGAGCAGTCGGGACACCGATT  
TATAAATAAAACTGAGCACCTTCTTTAAACAAAAA  
AAAAAAAAA

**FIGURE 4**

TGCCGGGCTGCGGGCGCCTGACTCTCCCTCACCCCTGCCTCCTCGGGCTCCACTCGTCTGCCCTGGACTCCC  
 GTCTCCTCCTGTCCTCCGGCTCCCAGAGCTCCCTCCTATGGCAGCAGCTTCCCGCGTCTCCGGCGCAGCTTCT  
 CAGCGGACGACCCCTCGCTCCGGGCTGAGCCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGGG  
 TTTGGCTGCTGCTTCCCAGCCACTGCCACCGCCGCCCTGCTGCCGCGTCCGGGATGCTCAG  
 TAGCCCCTGCCCGCCCCCGCATCCTGTGTTCTCGGAAGCCGTTGCTGCTGCCAGAGTTGCACGAACAGTC  
**ATG**GTGCTGTTGGAGTCCCAGGCAGTGCAGCAGCTGGACACTTGCAGGGCTTGCTGGCTGCTGCTGCTG  
 CCCGTCACTGCTACTCATCGTAGCCCGCCCGTGAAGCTCGCTGCTTCCCTACCTCTTAAGTGA  
 CTGCCAAACG  
 CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTCCTGTGACACCAACACCTGTA  
 TTTGATGGGAATGTTAAGAATTGGAGACACTGTGACTTGCCTGTCAGTTCAAGTGA  
 CAAACAATGACTATG  
 CCTGTGTGCTCCAATGGGAGAGCTACAGAATGAGTGTACCTGCGACAGGCTGCATGCCAAACAGCAGAGT  
 GAGATACTGTGGTGTGACAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGG  
 TCTGGAGAAACTAGTC  
 AAAAGGAGACATCCACCTGTGATATTGCCAGTTGGTGCAGAATGTGACGAAGATGCC  
 GAGGATGTC  
 GTGGTGTGTAATATTGACTGTTCTCAAACCAACTTC  
 AAATCCCCTGCGCTTCTGATGGAA  
 TCTTATGATAATGCATGCCAAATCAAAGAACATCGTGTGAGAACAGGAGAAAATTGAAGTCA  
 TGTCTTGGGT  
 CGATGTCAAGATAACACAACTACA  
 ACTAAGTCTGAAGATGGCATTATGCAAGAACAGATTATGCAGAGAAT  
 GCTAACAAATTAGAAGAAAGTGC  
 CAGAGAACACCACATACCTGTCCGGAACATTACA  
 ATGGCTTCTGCATGCAT  
 GGGAA  
 GTGAGCATTCTATCAATATGCAGGAGCCATCTGCAGGTGTGATGCTGGTTACTGGACAA  
 ACTGT  
 GAAAAAAAGGACTACAGTGTCTATACGGTGTCCGGTCTGTACGATT  
 CAGTATGCTTAATCGCAGCTGTG  
 ATTGGAA  
 ACAATT  
 CAGATTGCTGTCATCTGTG  
 GGTGCTCTGCAT  
 CACAAGGAA  
 ATGCC  
 CAGAAGCA  
 AACAGA  
 ATT  
 CACAGACAGAAC  
 AACACAGGGCA  
 ACTACAG  
 TT  
 CAGACA  
 ATACA  
 AACAGAGCGTCC  
 CAGAGGTT  
 ATCTAA  
**TAA**  
 AGGGAGCAT  
 GTTC  
 CACAGTGGCTGGACTACCGAGAGCTGGACTACACA  
 ATACAGTATT  
 ATAGAC  
 AAAAGA  
 ATAA  
 GACAAGAGATCT  
 ACACAT  
 GTTGC  
 CCTTG  
 CATT  
 GTGTA  
 ATCT  
 ACACCA  
 ATG  
 GAAA  
 ACAT  
 GT  
 ACTACAG  
 CTAT  
 ATT  
 GATT  
 ATG  
 TGT  
 GG  
 AT  
 ATT  
 TG  
 GAA  
 AT  
 AGT  
 AT  
 AC  
 ATT  
 GT  
 CTT  
 GT  
 G  
 T  
 T  
 CT  
 GT  
 TA  
 AT  
 GT  
 AA  
 AT  
 AA  
 ACT  
 ATT  
 TATA  
 T  
 AC  
 AC  
 AA  
 AT  
 AG  
 TT  
 TT  
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 CC  
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 ATT  
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 GT  
 TA  
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 TA  
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 AA  
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 AC  
 T  
 CAG  
 T  
 G  
 AT  
 G  
 G  
 A

**FIGURE 5**

TTCTGCTATAGAGATGGAACAGTATATGAAAGCTCCCAAGAAAGTGAAGAGAGGAAATTGAAAATTGTGAGTG  
 GACCTCTGATACTGCTCCTCGTGGAAAGGGAAAGAACTGCATGCATATTATTACAGCGCCTATATT  
 AAAGGATATTCTGGTATCTTGGAAAGTGTCCGTATC**ATGGA**ATCAATCTATGATGGAAAGCCCTAAGAGCCT  
 TAGTGAAACTGTGTTACCTAATGGCATAAATGGTATCAAAGATGCAAGGAAGGTCACTGTAGGTGTGATTGAAAG  
 TGGAGATTTGCCAAATCCTGACCATTGACTTATTAGATGCGGCTATCATGTGGTCAAGGAAGTAGAAATCC  
 TAAGTTGCTCTGAATTTTCCTCATGTGGTAGATGTCACTCATGAAGATGCTCTCACAAAACAAATAT  
 AATATTGTTGCTATACACAGAGAACATTACCTCCCTGTGGGACCTGAGACATCTGCTGTGGTAAATCCT  
 GATTGATGTGAGCAATAACATGAGGATAAACAGTACCCAGAATCCAATGCTGAATATTGGCTTATTATC  
 AGATTCTTGATTGTCAAAGGATTAATGTTGTCAGCTTGGGCACTTCAGTTAGGACCTAAGGATGCCAGCCG  
 GCAGGTTATATATGCAGCAACAATATTCAAGCGCAGAACAGGTTATTGAACCTGCCGCCAGTTGAATTTCAT  
 TCCCATTGACTTGGGATCCTTATCATCAGCCAGAGAGATTGAAAATTACCCCTACGACTCTTACTCTGGAG  
 AGGGCCAGTGGTAGCTATAAGCTTGGCACATTTCCTTATTGTCAGAGATGTGATTCA  
 ATATGCTAGAAACCAACAGAGTACTTTACAAAATTCTATAGAGATTGTGAATAAAACCTACCTATAGTTGC  
 CATTACTTGCTCTCCTAGTATACCTGCAGGTCTCTGGCAGCTGCTTACACTTATTACGGCACCAAGTA  
 TAGGAGATTCCACCTGGTTGAAACCTGGTTACAGTGTAGAAAACAGCTTGGATTACTAAGTTTTCTCGC  
 TATGGTCATGGCCTACAGCCTCTGCTTACCGATGAGAAGGTCAAGAGAGATTGTTGAGAATTGAAATGTATATCTC  
 TGGCATAATGAGCCTGGCTTACCTCCCTGGCAGTCACCTCTATCCCTCAGTGAGCAATGCTTAAACTG  
 GAGAGAATTCACTTATTCACTGAGTACACACTGGATATGTCGCTCTGCTCATAAGTACTTCCATGTTAATT  
 TGGATGGAAACGAGCTTGAGGAAGAGTACTACAGATTATACACCAACACTTGTCTGCTCTGTT  
 GCCCTCAATTGTAATTCTGGATCTTGCAGCTTGCAGATAACCCAGACT**TGA**GCTGGAACCTGAAATTGCTTCC  
 TATTGACTCTACTTCTTAAAGCGGCTGCCATTACATTCCCTAGCTGCTTGCAGTTAGGTGTACATGTGAC  
 TGAGTGTGGCAGTGGATATAACAGGAGCCCTGGCAGCTGCTCCAGAGGATCAAAGCCACACCCAAAGAGTAAGGCAG  
 ATTAGAGACCAGAAAGACCTTGACTACTCCACTGCTTTCTGCATTAAAGCCATTGAAATCTG  
 GGTGTGTTACATGAAGTGAAATTAAATTCTTCTGCCCTCAGTTCTTATCCTGATACCATTAAACACTGTCTG  
 AATTAAACTAGACTGCAATAATTCTTCTTTGAAAGCTTTAAAGGATAATGTGCAATTACATTAAATTGATT  
 TTCCATTGTCATTAGTTATACCTCATTCTGCCTGATCTTCATTAGATATTGTATCTGCTTGGAAATATA  
 TTATCTTCTTTAACTGTGTAATTGGTAATTACTAAAACCTGTAATCTCCAAATATTGCTATCAAATTACAC  
 ACCATGTTCTATCATTCTCATAGATCTGCCTATAAACATTAAATAAAAGTACTATTAAATGATTAACTT  
 CTGTTTGAAAAA

## **FIGURE 6**

MASLGLQLVGYILGLLGLGTIVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCDIYSTLLGLPA  
DIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGLGFIPVAWLHGILRDFYSP  
LVPDSMKFEIGEALYLGISSILFSLIAGIILCFSCSSQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYS  
LTGYV

**Signal sequence.**

amino acids 1-24

**Transmembrane domains.**

amino acids 82-102, 120-140, 160-180

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 216-224

**N-myristoylation sites.**

amino acids 17-22, 20-25, 60-65, 101-106, 128-133, 167-172, 178-183

**PMP-22/EMP/MP20/Claudin family.**

amino acids 4-181

**FIGURE 7**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIGPRKQ  
LCDGELDCPLGEDEEHCVKSFPPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETACRQMGYSRAVE  
IGPDQDLDVVVEITENSQELRMRNSSGPGCLSGSLVSLHCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVC  
GGSILDPHWVLTAAHCFRKHTDVFNWVKRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNNDIALMKLQFPLTFSGT  
VRPICLPPFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGV  
DTCQGDGGPLMYQSDQWHVVGIVSWGYPGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain.**

amino acids 33-60

**Trypsin.**

amino acids 200-424

**Kringle domain proteins.**

amino acids 225-242, 376-388

**Apple domain proteins.**

amino acids 199-239, 196-236, 237-270, 298-328, 368-401, 367-400, 403-430

**LDL-receptor class A.**

amino acids 70-89

**CUB domain proteins.**

amino acids 397-406

## FIGURE 8

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG  
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF  
SMPEVNVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSC  
MIENDIAKATGDIKVTESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYIMLK

**Signal peptide.**

amino acids 1-28

**Transmembrane domain.**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220, 220-224

**N-myristylation sites.**

amino acids 52-58, 126-132, 188-194

**Immunoglobulin domain.**

amino acids 49-132

## FIGURE 9

MVLWESPRQCSSWTLCEGFCWLLLLPVMLLIVARPVKLAAFPTSLSDCQPTGWNCSGYDDRENDLFLCDNTCK  
FDGECLRIGDTVTCVCQFKCNDYVPVCGSNGESYQNECYLRQAACKQQSEILVVSEGSCATDAGSGSGDGVHEG  
SGETSQKETSTCDICQFGAECDEDAEDVWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLG  
RCQDNNTTTKSEDGHYARTDYAENANKLEESAREHHIPCPHYNGFCMHGKCEHSINMQEPSCRCDAGYTGQHC  
EKKDYSVLYVVPGPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQKQNTGHYSSDNTRASTRLI

**N-glycosylation sites.**

amino acids 55-58, 230-233, 365-368

**Glycosaminoglycan attachment sites.**

amino acids 141-144, 143-146

**Tyrosine kinase phosphorylation site.**

amino acids 236-242

**N-myristoylation sites.**

amino acids 133-138, 140-145, 142-147, 146-151, 150-155

**EGF-like domain cysteine pattern signature.**

amino acids 289-301

**Kazal-type serine protease inhibitor domain.**

amino acids 91-135, 182-227

## **FIGURE 10**

MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPFASEFFPHVVD  
VTHHEDALTKTNIIFVAIHREHYTSIWDLRHLVGKILIDVSNNMRINQYPSNAEYLASLFPDSLIVKGFNVVS  
AWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIIDLGSLSAREIENPLRLFTLWRGPVVVAISLATF  
FFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAILLISLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLIQ  
CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNNEEVWRIEMYISFGIMSLGLLSLLA  
VTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYWKRAFEEYYRFYTPPNFVLALVLP SIVILDLLQLC  
RYPD

**Transmembrane domains.**

amino acids 210-230, 257-277, 299-319, 359-379, 393-413, 428-448

**N-glycosylation site.**

amino acids 256-259

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 29-32

**Tyrosine kinase phosphorylation site.**

amino acids 416-424

**N-myristoylation sites.**

amino acids 8-13, 24-29, 34-39, 193-198, 274-279